

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ozenberger, Brad A.
Jacobsen, J. S.
Kajkowski, Eileen
- (ii) TITLE OF INVENTION: β -Amyloid Peptide-Binding Proteins
and Polynucleotides Encoding the Same
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: American Home Products
 - (B) STREET: One Campus Drive
 - (C) CITY: Parsippany
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 07054
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Walsh, Andrea C.
 - (B) REGISTRATION NUMBER: 34,988
 - (C) REFERENCE/DOCKET NUMBER: 98126
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 973-683-2169
 - (B) TELEFAX: 973-683-4117

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 810 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: mRNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..807
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

09060609 041599

ATG	CAT	ATT	TTA	AAA	GGG	TCT	CCC	AAT	GTG	ATT	CCA	CGG	GCT	CAC	GGG	48
Met	His	Ile	Leu	Lys	Gly	Ser	Pro	Asn	Val	Ile	Pro	Arg	Ala	His	Gly	
1				5				10				15				
CAG	AAG	AAC	ACG	CGA	AGA	GAC	GGA	ACT	GGC	CTC	TAT	CCT	ATG	CGA	GGT	96
Gln	Lys	Asn	Thr	Arg	Arg	Asp	Gly	Thr	Gly	Leu	Tyr	Pro	Met	Arg	Gly	
20				25				30								
CCC	TTT	AAG	AAC	CTC	GCC	CTG	TTG	CCC	TTC	TCC	CTC	CCG	CTC	CTG	GGC	144
Pro	Phe	Lys	Asn	Leu	Ala	Leu	Leu	Pro	Phe	Ser	Leu	Pro	Leu	Leu	Gly	
35				40				45								
GGA	GGC	GGA	AGC	GGA	AGT	GGC	GAG	AAA	GTG	TCG	GTC	TCC	AAG	ATG	GCG	192
Gly	Gly	Gly	Ser	Gly	Ser	Gly	Glu	Lys	Val	Ser	Val	Ser	Lys	Met	Ala	
50				55				60								
GCC	GCC	TGG	CCG	TCT	GGT	CCG	TCT	GCT	CCG	GAG	GCC	GTG	ACG	GCC	AGA	240
Ala	Ala	Trp	Pro	Ser	Gly	Pro	Ser	Ala	Pro	Glu	Ala	Val	Thr	Ala	Arg	
65				70				75				80				
CTC	GTT	GGT	GTC	CTG	TGG	TTC	GTC	TCA	GTC	ACT	ACA	GGA	CCC	TGG	GGG	288
Leu	Val	Gly	Val	Leu	Trp	Phe	Val	Ser	Val	Thr	Thr	Gly	Pro	Trp	Gly	
85				90				95								
GCT	GTT	GCC	ACC	TCC	GCC	GGG	GGC	GAG	GAG	TCG	CTT	AAG	TGC	GAG	GAC	336
Ala	Val	Ala	Thr	Ser	Ala	Gly	Gly	Glu	Glu	Ser	Leu	Lys	Cys	Glu	Asp	
100				105				110								
CTC	AAA	GTG	GGA	CAA	TAT	ATT	TGT	AAA	GAT	CCA	AAA	ATA	AAT	GAC	GCT	384
Leu	Lys	Val	Gly	Gln	Tyr	Ile	Cys	Lys	Asp	Pro	Lys	Ile	Asn	Asp	Ala	
115				120				125								
ACG	CAA	GAA	CCA	GTT	AAC	TGT	ACA	AAC	TAC	ACA	GCT	CAT	GTT	TCC	TGT	432
Thr	Gln	Glu	Pro	Val	Asn	Cys	Thr	Asn	Tyr	Thr	Ala	His	Val	Ser	Cys	
130				135				140								
TTT	CCA	GCA	CCC	AAC	ATA	ACT	TGT	AAG	GAT	TCC	AGT	GGC	AAT	GAA	ACA	480
Phe	Pro	Ala	Pro	Asn	Ile	Thr	Cys	Lys	Asp	Ser	Ser	Gly	Asn	Glu	Thr	
145				150				155				160				
CAT	TTT	ACT	GGG	AAC	GAA	GTT	GGT	TTT	TTC	AAG	CCC	ATA	TCT	TGC	CGA	528
His	Phe	Thr	Gly	Asn	Glu	Val	Gly	Phe	Phe	Lys	Pro	Ile	Ser	Cys	Arg	
165				170				175								
AAT	GTA	AAT	GGC	TAT	TCC	TAC	AAA	GTG	GCA	GTC	GCA	TTG	TCT	CTT	TTT	576
Asn	Val	Asn	Gly	Tyr	Ser	Tyr	Lys	Val	Ala	Val	Ala	Leu	Ser	Leu	Phe	
180				185				190								
CTT	GGA	TGG	TTG	GGA	GCA	GAT	CGA	TTT	TAC	CTT	GGA	TAC	CCT	GCT	TTG	624
Leu	Gly	Trp	Leu	Gly	Ala	Asp	Arg	Phe	Tyr	Leu	Gly	Tyr	Pro	Ala	Leu	
195				200				205								
GGT	TTG	TTA	AAG	TTT	TGC	ACT	GTA	GGG	TTT	TGT	GGA	ATT	GGG	AGC	CTA	672
Gly	Leu	Leu	Lys	Phe	Cys	Thr	Val	Gly	Phe	Cys	Gly	Ile	Gly	Ser	Leu	
210				215				220								
ATT	GAT	TTC	ATT	CTT	ATT	TCA	ATG	CAG	ATT	GTT	GGA	CCT	TCA	GAT	GGA	720

															44															
Ile	Asp	Phe	Ile	Leu	Ile	Ser	Met	Gln	Ile	Val	Gly	Pro	Ser	Asp	Gly															
225					230					235					240															
AGT	AGT	TAC	ATT	ATA	GAT	TAC	TAT	GGA	ACC	AGA	CTT	ACA	AGA	CTG	AGT	768														
Ser	Ser	Tyr	Ile	Ile	Asp	Tyr	Tyr	Gly	Thr	Arg	Leu	Thr	Arg	Leu	Ser															
				245					250					255																
ATT	ACT	AAT	GAA	ACA	TTT	AGA	AAA	ACG	CAA	TTA	TAT	CCA	TAA																	
Ile	Thr	Asn	Glu	Thr	Phe	Arg	Lys	Thr	Gln	Leu	Tyr	Pro																		
				260					265																					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	His	Ile	Leu	Lys	Gly	Ser	Pro	Asn	Val	Ile	Pro	Arg	Ala	His	Gly
1				5					10					15	
Gln	Lys	Asn	Thr	Arg	Arg	Asp	Gly	Thr	Gly	Leu	Tyr	Pro	Met	Arg	Gly
			20					25					30		
Pro	Phe	Lys	Asn	Leu	Ala	Leu	Leu	Pro	Phe	Ser	Leu	Pro	Leu	Leu	Gly
		35					40					45			
Gly	Gly	Gly	Ser	Gly	Ser	Gly	Glu	Lys	Val	Ser	Val	Ser	Lys	Met	Ala
	50					55					60				
Ala	Ala	Trp	Pro	Ser	Gly	Pro	Ser	Ala	Pro	Glu	Ala	Val	Thr	Ala	Arg
65					70					75					80
Leu	Val	Gly	Val	Leu	Trp	Phe	Val	Ser	Val	Thr	Thr	Gly	Pro	Trp	Gly
				85					90					95	
Ala	Val	Ala	Thr	Ser	Ala	Gly	Gly	Glu	Glu	Ser	Leu	Lys	Cys	Glu	Asp
			100					105					110		
Leu	Lys	Val	Gly	Gln	Tyr	Ile	Cys	Lys	Asp	Pro	Lys	Ile	Asn	Asp	Ala
		115					120					125			
Thr	Gln	Glu	Pro	Val	Asn	Cys	Thr	Asn	Tyr	Thr	Ala	His	Val	Ser	Cys
	130					135					140				
Phe	Pro	Ala	Pro	Asn	Ile	Thr	Cys	Lys	Asp	Ser	Ser	Gly	Asn	Glu	Thr
145					150					155					160
His	Phe	Thr	Gly	Asn	Glu	Val	Gly	Phe	Phe	Lys	Pro	Ile	Ser	Cys	Arg
				165					170					175	
Asn	Val	Asn	Gly	Tyr	Ser	Tyr	Lys	Val	Ala	Val	Ala	Leu	Ser	Leu	Phe
			180					185					190		

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Met	His	Ile	Leu	Lys	Gly	Ser	Pro	Asn	Val	Ile	Pro	Arg	Ala	His	Gly	
1				5				10						15		
CAG	AAG	AAC	ACG	CGA	AGA	GAC	GGA	ACT	GGC	CTC	TAT	CCT	ATG	CGA	GGT	96

Gln	Lys	Asn	Thr 20	Arg	Arg	Asp	Gly	Thr 25	Gly	Leu	Tyr	Pro	Met 30	Arg	Gly	
CCC Pro	TTT Phe	AAG Lys 35	AAC Asn	CTC Leu	GCC Ala	CTG Leu	TTG Leu 40	CCC Pro	TTC Phe	TCC Ser	CTC Leu	CCG Pro 45	CTC Leu	CTG Leu	GGC Gly	144
GGA Gly	GGC Gly 50	GGA Gly	AGC Ser	GGA Gly	AGT Ser	GGC Gly 55	GAG Glu	AAA Lys	GTG Val	TCG Ser	GTC Val 60	TCC Ser	AAG Lys	ATG Met	GCG Ala	192
GCC Ala 65	GCC Ala	TGG Trp	CCG Pro	TCT Ser	GGT Gly 70	CCG Pro	TCT Ser	GCT Ala	CCG Pro	GAG Glu 75	GCC Ala	GTG Val	ACG Thr	GCC Ala	AGA Arg 80	240
CTC Leu	GTT Val	GGT Gly	GTC Val	CTG Leu 85	TGG Trp	TTC Phe	GTC Val	TCA Ser	GTC Val 90	ACT Thr	ACA Thr	GGA Gly	CCC Pro	TGG Trp 95	GGG Gly	288
GCT Ala	GTT Val	GCC Ala	ACC Thr 100	TCC Ser	GCC Ala	GGG Gly	GGC Gly	GAG Glu 105	GAG Glu	TCG Ser	CTT Leu	AAG Lys	TGC Cys 110	GAG Glu	GAC Asp	336
CTC Leu	AAA Lys	GTG Val 115	GGA Gly	CAA Gln	TAT Tyr	ATT Ile	TGT Cys 120	AAA Lys	GAT Asp	CCA Pro	AAA Lys	ATA Ile 125	AAT Asn	GAC Asp	GCT Ala	384
ACG Thr	CAA Gln 130	GAA Glu	CCA Pro	GTT Val	AAC Asn	TGT Cys 135	ACA Thr	AAC Asn	TAC Tyr	ACA Thr	GCT Ala 140	CAT His	GTT Val	TCC Ser	TGT Cys	432
TTT Phe 145	CCA Pro	GCA Ala	CCC Pro	AAC Asn	ATA Ile 150	ACT Thr	TGT Cys	AAG Lys	GAT Asp	TCC Ser 155	AGT Ser	GGC Gly	AAT Asn	GAA Glu	ACA Thr 160	480
CAT His	TTT Phe	ACT Thr	GGG Gly	AAC Asn 165	GAA Glu	GTT Val	GGT Gly	TTT Phe 170	TTC Phe	AAG Lys	CCC Pro	ATA Ile	TCT Ser	TGC Cys 175	CGA Arg	528
AAT Asn	GTA Val	AAT Asn	GGC Gly 180	TAT Tyr	TCC Ser	TAC Tyr	AAA Lys 185	GTG Val	GCA Ala	GTC Val	GCA Ala	TTG Leu	TCT Ser 190	CTT Leu	TTT Phe	576
CTT Leu	GGA Gly	TGG Trp 195	TTG Leu	GGA Gly	GCA Ala	GAT Asp	CGA Arg 200	TTT Phe	TAC Tyr	CTT Leu	GGA Gly 205	TAC Tyr	CCT Pro	GCT Ala	TTG Leu	624
GGT Gly	TTG Leu 210	TTA Leu	AAG Lys	TTT Phe	TGC Cys	ACT Thr 215	GTA Val	GGG Gly	TTT Phe	TGT Cys	GGA Gly 220	ATT Ile	GGG Gly	AGC Ser	CTA Leu	672
ATT Ile 225	GAT Asp	TTC Phe	ATT Ile	CTT Leu	ATT Ile 230	TCA Ser	ATG Met	CAG Gln	ATT Ile	GTT Val 235	GGA Gly	CCT Pro	TCA Ser	GAT Asp	GGA Gly 240	720
AGT Ser	AGT Ser	TAC Tyr	ATT Ile	ATA Ile 245	GAT Asp	TAC Tyr	TAT Tyr	GGA Gly	ACC Thr 250	AGA Arg	CTT Leu	ACA Thr	AGA Arg	CTG Leu 255	AGT Ser	768
ATT Ile	ACT Thr	AAT Asn	GAA Glu 260	ACA Thr	TTT Phe	AGA Arg	AAA Lys	ACG Thr 265	CAA Gln	TTA Leu	TAT Tyr	CCA Pro	TAA			810

(2) INFORMATION FOR SEQ ID NO:2:

[illegible]

(B) TYPE: amino acid

Met 1	His	Ile	Leu	Lys 5	Gly	Ser	Pro	Asn	Val 10	Ile	Pro	Arg	Ala	His 15	Gly
Gln	Lys	Asn	Thr 20	Arg	Arg	Asp	Gly	Thr 25	Gly	Leu	Tyr	Pro	Met 30	Arg	Gly
Pro	Phe	Lys 35	Asn	Leu	Ala	Leu	Leu 40	Pro	Phe	Ser	Leu	Pro 45	Leu	Leu	Gly
Gly	Gly 50	Gly	Ser	Gly	Ser	Gly 55	Glu	Lys	Val	Ser	Val 60	Ser	Lys	Met	Ala
Ala 65	Ala	Trp	Pro	Ser	Gly 70	Pro	Ser	Ala	Pro	Glu 75	Ala	Val	Thr	Ala	Arg 80
Leu	Val	Gly	Val	Leu 85	Trp	Phe	Val	Ser	Val 90	Thr	Thr	Gly	Pro	Trp 95	Gly
Ala	Val	Ala	Thr 100	Ser	Ala	Gly	Gly	Glu 105	Glu	Ser	Leu	Lys	Cys 110	Glu	Asp
Leu	Lys	Val 115	Gly	Gln	Tyr	Ile	Cys 120	Lys	Asp	Pro	Lys	Ile 125	Asn	Asp	Ala
Thr	Gln 130	Glu	Pro	Val	Asn	Cys 135	Thr	Asn	Tyr	Thr	Ala 140	His	Val	Ser	Cys
Phe 145	Pro	Ala	Pro	Asn	Ile 150	Thr	Cys	Lys	Asp	Ser 155	Ser	Gly	Asn	Glu	Thr 160
His	Phe	Thr	Gly	Asn 165	Glu	Val	Gly	Phe	Phe 170	Lys	Pro	Ile	Ser	Cys 175	Arg
Asn	Val	Asn	Gly 180	Tyr	Ser	Tyr	Lys	Val 185	Ala	Val	Ala	Leu	Ser 190	Leu	Phe
Leu	Gly	Trp 195	Leu	Gly	Ala	Asp	Arg 200	Phe	Tyr	Leu	Gly	Tyr 205	Pro	Ala	Leu
Gly	Leu 210	Leu	Lys	Phe	Cys	Thr 215	Val	Gly	Phe	Cys	Gly 220	Ile	Gly	Ser	Leu
Ile 225	Asp	Phe	Ile	Leu	Ile 230	Ser	Met	Gln	Ile	Val 235	Gly	Pro	Ser	Asp	Gly 240
Ser	Ser	Tyr	Ile	Ile 245	Asp	Tyr	Tyr	Gly	Thr 250	Arg	Leu	Thr	Arg	Leu 255	Ser
Ile	Thr	Asn	Glu 260	Thr	Phe	Arg	Lys	Thr 265	Gln	Leu	Tyr	Pro			